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INTERACTION BETWEEN MAIZE RIBOSOME-INACTIVATING PROTEIN AND RIBOSOMES

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Ribosome-inactivating proteins (RIPs) represent a group of N-glycosidases which can cleave the N-glycosidic bond of adenine at 23S and 28S ribosomal RNA (rRNA) of ribosome and subsequently lead to a halt of protein synthesis and cell death.

Regardless to the universal rRNA target, the highly conserved catalytic residues and consensus tertiary structure of RIPs, the activity of RIPs is highly deviated. It is known that interacting with ribosomal proteins is required before RIPs elicit their direct action on rRNA. Here we hypothesize the interaction between RIPs and ribosome is correlated to the activity of RIPs.

In this study, we compared the catalytic activity of three RIPs: maize RIP (MOD), trichosanthin (TCS) and ricin A chain (RTA) and the nature of the interaction with their common ribosomal interacting partner, the stalk protein P2. Using pull-down assay and surface plasmon resonance, we found that MOD interacts with P2 chiefly through electrostatic interaction whilst TCS and RTA via a combination of electrostatic and hydrophobic forces. MOD-P2 is the weakest pair as revealed from its highest binding affinity constant (K_D) of 1 μM. TCS interacts with P2 relatively stronger at a K_D of 0.61 μM but is weaker than RTA-P2 which has a K_D of 0.24 μM. The pattern is also coincident with their *N*-glycosidase activity on rat liver ribosome and cytotoxicity on JAR and 293T cells. We conclude that RIPs despite targeting at the same ribosomal protein, the nature of the interaction is the crucial factor of the strength of their interaction and activity.